SCORE Search Results Details for

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This page gives you Search Results detail for the Application 10718495 and Search Result us-10-7:
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 25, 2006, 14:10:57 ; Search time 23.698 Seconds
(without alignments)
856.686 Million cell updates/sec

Title: US-10-718-495-25
Perfect score: 1131
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....EDEEDEEEEDEEDEEDDDDE 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1064	94.1	215	1	S01947	nonhistone chromos
2	1061	93.8	215	2	S02826	nonhistone chromos
3	1059	93.6	215	2	A28897	nonhistone chromos
4	1058	93.5	215	1	NSRTH1	nonhistone chromos
5	1058	93.5	215	2	I48688	non-histone chromo
6	1045	92.4	216	2	S29857	nonhistone chromos
7	959.5	84.8	210	2	S62355	high mobility grou
8	883	78.1	210	2	A34719	nonhistone chromos

9	876	77.5	210	2	S54774	high mobility grou
10	875.5	77.4	209	1	NSHUH2	nonhistone chromos
11	863	76.3	207	2	JC1114	high-mobility grou
12	853	75.4	207	2	JC1129	nonhistone chromos
13	823	72.8	170	2	A27853	nonhistone chromos
14	798.5	70.6	204	2	S48708	high-mobility-grou
15	791.5	70.0	204	2	T01071	high mobility grou
16	779.5	68.9	202	2	S22359	nonhistone chromos
17	779.5	68.9	205	2	S26062	nonhistone chromos
18	764	67.6	201	2	I50254	HMG-1 - chicken
19	750.5	66.4	186	2	S30221	nonhistone chromos
20	735	65.0	186	2	B61611	nonhistone chromos
21	719	63.6	215	2	I51067	gene HMG-T2 protei
22	655	57.9	172	2	A24019	nonhistone chromos
23	514	45.4	393	2	S50068	nonhistone chromos
24	511	45.2	393	2	JC6179	dorsal switch prot
25	456	40.3	200	2	JC4357	HMG1 protein - sea
26	335	29.6	202	2	E88479	protein F47D12.4 [
27	326	28.8	235	2	T43009	HMG protein 1.2 -
28	296	26.2	662	2	F86339	protein F2D10.18 [
29	288	25.5	168	2	T03640	high mobility grou
30	287	25.4	157	2	B47150	high mobility grou
31	273	24.1	178	2	T51159	HMG protein [impor
32	261	23.1	161	2	S18991	high mobility grou
33	258	22.8	54	2	S68823	HMG1 protein homol
34	257	22.7	141	2	T09581	probable high mobi
35	254.5	22.5	149	2	S39556	high mobility grou
36	253.5	22.4	144	2	S40302	high mobility grou
37	253.5	22.4	502	2	T14286	embryogenic callus
38	253	22.4	708	2	A41265	DNA-binding protei
39	251.5	22.2	669	2	S78050	high mobility grou
40	244.5	21.6	142	2	T02252	high mobility grou
41	242.5	21.4	709	2	A41976	structure-specific
42	236.5	20.9	561	2	S35637	high mobility grou
43	232.5	20.6	154	2	S40122	high mobility grou
44	232	20.5	141	2	T51598	high mobility grou
45	232	20.5	144	2	T51597	high mobility grou

ALIGNMENTS

RESULT 1
S01947
nonhistone chromosomal protein HMG-1 - bovine
N;Alternate names: 33K protein; high-mobility-group protein HMG-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: S01947; A61611; S10959; I45910
R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: S01947; MUID:89057489; PMID:3194213
A;Accession: S01947
A;Molecule type: mRNA
A;Residues: 1-215
A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; NID:g416; PIDN
R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
FEBS Lett. 122, 264-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: A61611; MUID:81138848; PMID:7202717

SCORE Search Results Details for Applicatio 10718495 and Search Result us-10-718-495-25.r

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10718495 and Search Result us-10-7: 25.rapbn.

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 25, 2006, 14:20:33 ; Search time 17.3785 Seconds
(without alignments)
534.258 Million cell updates/sec

Title: US-10-718-495-25
Perfect score: 1131
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....EDEEDEEEEDEEDEEDDDDE 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1061	93.8	215	6	US-10-821-234-1443	Sequence 1443, Ap

2	1061	93.8	215	7	US-11-186-422-11	Sequence 11, Appl
3	1058	93.5	215	7	US-11-186-422-12	Sequence 12, Appl
4	790.5	69.9	879	7	US-11-169-041-192	Sequence 192, App
5	641	56.7	169	6	US-10-821-234-1234	Sequence 1234, Ap
6	355	31.4	69	7	US-11-186-422-14	Sequence 14, Appl
7	263	23.3	54	6	US-10-719-150-6	Sequence 6, Appli
8	263	23.3	54	7	US-11-186-422-13	Sequence 13, Appl
9	263	23.3	146	7	US-11-172-740-1569	Sequence 1569, Ap
10	257	22.7	141	7	US-11-087-099-3073	Sequence 3073, Ap
11	254.5	22.5	149	7	US-11-087-099-3510	Sequence 3510, Ap
12	254.5	22.5	149	7	US-11-172-740-1571	Sequence 1571, Ap
13	253.5	22.4	502	7	US-11-087-099-8879	Sequence 8879, Ap
14	249.5	22.1	160	7	US-11-087-099-1105	Sequence 1105, Ap
15	244.5	21.6	142	7	US-11-087-099-4976	Sequence 4976, Ap
16	243.5	21.5	388	7	US-11-087-099-4330	Sequence 4330, Ap
17	235	20.8	487	7	US-11-087-099-11126	Sequence 11126, A
18	232.5	20.6	154	7	US-11-087-099-2474	Sequence 2474, Ap
19	232.5	20.6	154	7	US-11-172-740-1570	Sequence 1570, Ap
20	232.5	20.6	380	7	US-11-087-099-5374	Sequence 5374, Ap
21	229	20.2	141	7	US-11-087-099-9185	Sequence 9185, Ap
22	228.5	20.2	187	7	US-11-096-568A-32735	Sequence 32735, A
23	228.5	20.2	241	7	US-11-096-568A-32734	Sequence 32734, A
24	228.5	20.2	257	7	US-11-096-568A-32733	Sequence 32733, A
25	228	20.2	446	7	US-11-087-099-370	Sequence 370, App
26	227	20.1	145	7	US-11-172-740-1572	Sequence 1572, Ap
27	226.5	20.0	372	7	US-11-087-099-6977	Sequence 6977, Ap
28	216	19.1	139	7	US-11-096-568A-13611	Sequence 13611, A
29	216	19.1	152	7	US-11-172-740-1565	Sequence 1565, Ap
30	214.5	19.0	139	7	US-11-096-568A-26884	Sequence 26884, A
31	214.5	19.0	152	7	US-11-087-099-313	Sequence 313, App
32	214.5	19.0	152	7	US-11-172-740-1566	Sequence 1566, Ap
33	214.5	19.0	187	7	US-11-096-568A-26883	Sequence 26883, A
34	213.5	18.9	140	7	US-11-172-740-1564	Sequence 1564, Ap
35	213	18.8	164	7	US-11-096-568A-3510	Sequence 3510, Ap
36	212	18.7	165	7	US-11-096-568A-21033	Sequence 21033, A
37	212	18.7	212	7	US-11-096-568A-21032	Sequence 21032, A
38	212	18.7	234	7	US-11-096-568A-21031	Sequence 21031, A
39	203.5	18.0	137	7	US-11-096-568A-3511	Sequence 3511, Ap
40	196	17.3	124	7	US-11-096-568A-9681	Sequence 9681, Ap
41	196	17.3	162	7	US-11-096-568A-9680	Sequence 9680, Ap
42	191	16.9	93	7	US-11-087-099-869	Sequence 869, App
43	190	16.8	93	7	US-11-087-099-9518	Sequence 9518, Ap
44	187.5	16.6	92	7	US-11-087-099-8838	Sequence 8838, Ap
45	187	16.5	487	7	US-11-124-368A-308	Sequence 308, App

ALIGNMENTS

```
RESULT 1
US-10-821-234-1443
; Sequence 1443, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
```

SCORE Search Results Details for Application 10718495 and Search Result us-10-718-495-25.rup.

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This page gives you Search Results detail for the Application 10718495 and Search Result us-10-718-495-25.rup.

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 25, 2006, 13:40:01 ; Search time 143.943 Seconds
(without alignments)
1034.201 Million cell updates/sec

Title: US-10-718-495-25
Perfect score: 1131
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....EDEEDEEEEDEEDEEDDDDE 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1131	100.0	211	2	Q9NQJ4_HUMAN	Q9nqj4 homo sapien
2	1061	93.8	215	2	Q5T7C3_HUMAN	Q5t7c3 homo sapien
3	1061	93.8	215	2	Q4R844_MACFA	Q4r844 macaca fasc
4	1059	93.6	214	1	HMG1_BOVIN	P10103 bos taurus

5	1058	93.5	215	2	Q548R9_RAT	Q548r9 rattus norv
6	1058	93.5	215	2	Q58EV5_MOUSE	Q58ev5 m high mobi
7	1057	93.5	215	2	Q9QX40_SPAEH	Q9qx40 spalax leuc
8	1056	93.4	214	1	HMG1_CANFA	Q6yka4 canis famil
9	1056	93.4	214	1	HMG1_HUMAN	P09429 homo sapien
10	1054	93.2	214	1	HMG1_PIG	P12682 sus scrofa
11	1054	93.2	215	2	O88612_SPAEH	O88612 spalax leuc
12	1054	93.2	215	2	Q9QWY6_SPAEH	Q9qwy6 spalax leuc
13	1053	93.1	214	1	HMG1_MOUSE	P63158 mus musculu
14	1053	93.1	214	1	HMG1_RAT	P63159 rattus norv
15	1052	93.0	215	2	Q6P202_MOUSE	Q6p202 mus musculu
16	1051	92.9	215	2	O88611_SPAEH	O88611 spalax leuc
17	1047	92.6	215	2	Q8BQ02_MOUSE	Q8bq02 mus musculu
18	1041	92.0	215	2	Q14321_HUMAN	Q14321 homo sapien
19	1023	90.5	211	1	HMG1X_HUMAN	Q9ugv6 homo sapien
20	1014	89.7	215	2	Q9YH06_CHICK	Q9yh06 gallus gall
21	1007.5	89.1	214	2	Q9PUK9_CHICK	Q9puk9 gallus gall
22	977	86.4	192	2	Q5T7C5_HUMAN	Q5t7c5 homo sapien
23	968	85.6	211	2	Q7SZ42_XENLA	Q7sz42 xenopus lae
24	967	85.5	206	2	Q5BKQ1_MOUSE	Q5bkq1 mus musculu
25	965	85.3	211	2	Q6P4N5_XENTR	Q6p4n5 xenopus tro
26	959.5	84.8	210	2	Q91596_XENLA	Q91596 xenopus lae
27	956.5	84.6	210	2	Q6GNQ5_XENLA	Q6gnq5 xenopus lae
28	921	81.4	181	2	Q8BNM0_MOUSE	Q8bnm0 mus musculu
29	907	80.2	178	2	Q8C7C4_MOUSE	Q8c7c4 mus musculu
30	878	77.6	209	1	HMG2_PIG	P17741 sus scrofa
31	875.5	77.4	209	2	Q5U072_HUMAN	Q5u072 homo sapien
32	874	77.3	208	2	Q5U071_HUMAN	Q5u071 homo sapien
33	874	77.3	210	2	Q5FVP0_RAT	Q5fvp0 rattus norv
34	872	77.1	180	1	HMG1_CRIGR	P07156 cricetulus
35	871	77.0	209	1	HMG2_MOUSE	P30681 mus musculu
36	870.5	77.0	208	1	HMG2_HUMAN	P26583 homo sapien
37	869	76.8	209	1	HMG2_RAT	P52925 rattus norv
38	864	76.4	191	2	Q75MM1_HUMAN	Q75mm1 homo sapien
39	859	76.0	212	2	Q7ZXK5_XENLA	Q7zxk5 xenopus lae
40	858	75.9	206	1	HMG2_CHICK	P26584 gallus gall
41	856	75.7	208	2	Q80YZ1_MOUSE	Q80yz1 mus musculu
42	849	75.1	212	2	Q8AVU3_XENLA	Q8avu3 xenopus lae
43	844.5	74.7	212	2	Q6P7M9_XENTR	Q6p7m9 xenopus tro
44	840	74.3	212	2	Q91764_XENLA	Q91764 xenopus lae
45	838.5	74.1	205	2	Q7ZVC6_BRARE	Q7zvc6 brachydanio

ALIGNMENTS

```
RESULT 1
Q9NQJ4_HUMAN
ID   Q9NQJ4_HUMAN PRELIMINARY;      PRT;   211 AA.
AC   Q9NQJ4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   OTTHUMP00000031372.
GN   Name=HMG1L1; ORFNames=RP4-579F20.2-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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SCORE Search Results Details for Application 10718495 and Search Result us-10-718-495-25.rai.

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This page gives you Search Results detail for the Application 10718495 and Search Result us-10-718-495-25.rai.

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                          GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          April 25, 2006, 14:13:17 ; Search time 36.5125 Seconds
                                            (without alignments)
                                            477.770 Million cell updates/sec

Title:           US-10-718-495-25
Perfect score:   1131
Sequence:        1 MGKGDPKKPRGKMSSYAFFV.........EDEEDEEEEDEEDEEDDDDE 211

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:      572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Issued_Patents_AA:*
                1:  /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                2:  /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                3:  /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                4:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                5:  /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES

                 %
Result           Query
   No.    Score  Match Length DB  ID                          Description
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1	1059	93.6	214	2	US-09-214-881A-3	Sequence 3, Appli
2	1056	93.4	214	2	US-09-538-092-883	Sequence 883, App
3	1056	93.4	214	2	US-09-214-881A-1	Sequence 1, Appli
4	1054	93.2	214	2	US-09-214-881A-4	Sequence 4, Appli
5	1051	92.9	214	2	US-09-214-881A-5	Sequence 5, Appli
6	1029	91.0	213	2	US-09-949-016-10813	Sequence 10813, A
7	878	77.6	209	2	US-09-214-881A-6	Sequence 6, Appli
8	875.5	77.4	320	2	US-09-949-016-10728	Sequence 10728, A
9	872	77.1	209	2	US-09-214-881A-8	Sequence 8, Appli
10	870.5	77.0	208	2	US-09-538-092-1018	Sequence 1018, Ap
11	870.5	77.0	208	2	US-09-214-881A-2	Sequence 2, Appli
12	848	75.0	206	2	US-09-214-881A-9	Sequence 9, Appli
13	790.5	69.9	879	2	US-09-914-259-38	Sequence 38, Appl
14	789.5	69.8	208	2	US-09-214-881A-11	Sequence 11, Appl
15	774.5	68.5	201	2	US-09-214-881A-10	Sequence 10, Appl
16	756.5	66.9	200	2	US-09-702-705-789	Sequence 789, App
17	756.5	66.9	200	2	US-09-736-457-789	Sequence 789, App
18	756.5	66.9	200	2	US-09-614-124B-789	Sequence 789, App
19	756.5	66.9	200	2	US-09-671-325-789	Sequence 789, App
20	756.5	66.9	200	2	US-09-589-184-789	Sequence 789, App
21	756.5	66.9	200	2	US-09-658-824-789	Sequence 789, App
22	756.5	66.9	200	2	US-10-017-754-789	Sequence 789, App
23	756.5	66.9	200	2	US-09-651-563-789	Sequence 789, App
24	756.5	66.9	200	2	US-09-519-642-789	Sequence 789, App
25	756.5	66.9	228	2	US-09-949-016-10496	Sequence 10496, A
26	751.5	66.4	207	2	US-09-702-705-1667	Sequence 1667, Ap
27	751.5	66.4	207	2	US-09-736-457-1667	Sequence 1667, Ap
28	751.5	66.4	207	2	US-09-614-124B-1667	Sequence 1667, Ap
29	751.5	66.4	207	2	US-09-671-325-1667	Sequence 1667, Ap
30	751.5	66.4	207	2	US-09-658-824-1667	Sequence 1667, Ap
31	751.5	66.4	207	2	US-10-017-754-1667	Sequence 1667, Ap
32	751.5	66.4	207	2	US-10-017-754-1913	Sequence 1913, Ap
33	751.5	66.4	207	2	US-09-651-563-1667	Sequence 1667, Ap
34	743.5	65.7	200	2	US-09-702-705-324	Sequence 324, App
35	743.5	65.7	200	2	US-09-736-457-324	Sequence 324, App
36	743.5	65.7	200	2	US-09-614-124B-324	Sequence 324, App
37	743.5	65.7	200	2	US-09-671-325-324	Sequence 324, App
38	743.5	65.7	200	2	US-09-589-184-324	Sequence 324, App
39	743.5	65.7	200	2	US-09-658-824-324	Sequence 324, App
40	743.5	65.7	200	2	US-10-017-754-324	Sequence 324, App
41	743.5	65.7	200	2	US-09-651-563-324	Sequence 324, App
42	743.5	65.7	200	2	US-09-519-642-324	Sequence 324, App
43	723.5	64.0	185	2	US-09-214-881A-7	Sequence 7, Appli
44	563	49.8	110	2	US-09-513-999C-4824	Sequence 4824, Ap
45	547	48.4	110	2	US-09-513-999C-4825	Sequence 4825, Ap

ALIGNMENTS

RESULT 1
US-09-214-881A-3
; Sequence 3, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa

SCORE Search Results Details for Application 10718495 and Search Result us-10-718-495-25.rag.

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This page gives you Search Results detail for the Application 10718495 and Search Result us-10-718-495-25.rag.

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 25, 2006, 13:39:32 ; Search time 150.614 Seconds
(without alignments)
615.540 Million cell updates/sec

Title: US-10-718-495-25
Perfect score: 1131
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....EDEEDEEEEDEEDEEDDDDE 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	1131	100.0	211	8	ADO25942	Ado25942 Human HMG
2	1131	100.0	211	8	ADO71501	Ado71501 Human hig
3	1131	100.0	211	9	ADY85337	Ady85337 High mobi
4	1061	93.8	215	6	ABU07499	Abu07499 Protein d
5	1061	93.8	215	6	AAE35859	Aae35859 Human HMG
6	1061	93.8	215	7	ADD40789	Add40789 Human HMG
7	1061	93.8	215	7	ADD40788	Add40788 Human HMG
8	1061	93.8	215	7	ABM85677	Abm85677 Human pro
9	1061	93.8	215	8	ADO60491	Ado60491 Human hig
10	1061	93.8	215	8	ADO25918	Ado25918 Human hig
11	1061	93.8	215	8	ADO71477	Ado71477 Human hig
12	1061	93.8	215	8	ADR45922	Adr45922 Human hig
13	1061	93.8	215	8	ABM81508	Abm81508 Tumour-as
14	1061	93.8	215	9	ADW81011	Adw81011 Amphoteri
15	1061	93.8	215	9	ADX69343	Adx69343 Human amp
16	1061	93.8	215	9	ADY14248	Ady14248 PRO polyp
17	1061	93.8	215	9	ADY85326	Ady85326 Human hig
18	1061	93.8	215	9	ADY85085	Ady85085 Human HMG
19	1061	93.8	215	9	ADZ80804	Adz80804 Amino aci
20	1058	93.5	215	5	ABB57220	Abb57220 Mouse isc
21	1058	93.5	215	6	AAE35860	Aae35860 Mouse and
22	1058	93.5	215	7	ADD47643	Add47643 Rat Prote
23	1058	93.5	215	8	ADO25919	Ado25919 Mouse/rat
24	1058	93.5	215	8	ADO71478	Ado71478 Mouse/rat
25	1058	93.5	215	8	ADR87104	Adr87104 High Mobi
26	1058	93.5	215	9	ADY85327	Ady85327 Mouse and
27	1058	93.5	220	7	ABM85676	Abm85676 Mouse pro
28	1058	93.5	252	9	ADY85016	Ady85016 Human HMG
29	1056	93.4	214	7	ADD47645	Add47645 Human Pro
30	1056	93.4	214	7	ADE60447	Ade60447 Human Pro
31	1056	93.4	214	7	ADE57980	Ade57980 Human Pro
32	1056	93.4	214	7	ADE57984	Ade57984 Human Pro
33	1056	93.4	214	7	ADE60732	Ade60732 Human Pro
34	1056	93.4	214	7	ADE60728	Ade60728 Human Pro
35	1056	93.4	214	8	ADS17580	Ads17580 Amino aci
36	1056	93.4	215	9	ADY85029	Ady85029 Rat and m
37	1056	93.4	215	9	ADY85088	Ady85088 Human HMG
38	1056	93.4	221	9	ADY85051	Ady85051 Human HMG
39	1054	93.2	229	5	ABP64829	Abp64829 Human pro
40	1053	93.1	214	7	ADE60730	Ade60730 Rat Prote
41	1053	93.1	214	7	ADE57978	Ade57978 Rat Prote
42	1053	93.1	214	7	ADE57982	Ade57982 Rat Prote
43	1053	93.1	214	7	ADE60726	Ade60726 Rat Prote
44	1053	93.1	214	7	ADE60445	Ade60445 Rat Prote
45	1052.5	93.1	213	8	ADP30030	Adp30030 Human sec

ALIGNMENTS

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ADO25942
ID   ADO25942 standard; protein; 211 AA.
XX
AC   ADO25942;
XX
DT   26-AUG-2004  (first entry)
XX
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SCORE Search Results Details for Application 10718495 and Search Result us-10-718-495-25.rapbm.

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This page gives you Search Results detail for the Application 10718495 and Search Result us-10-718-495-25.rapbm.

start

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```
                          GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          April 25, 2006, 14:19:43 ; Search time 120.07 Seconds
                                            (without alignments)
                                            734.256 Million cell updates/sec

Title:           US-10-718-495-25
Perfect score:   1131
Sequence:        1 MGKGDPKKPRGKMSSYAFFV.........EDEEDEEEEDEEDEEDDDDE 211

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:      1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_AA_Main:*
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                 2:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                 4:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 5:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 6:  /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES

                  %
Result            Query
   No.    Score   Match Length DB  ID                          Description
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1	1131	100.0	211	4	US-10-300-072-25	Sequence 25, Appl
2	1131	100.0	211	4	US-10-456-947-12	Sequence 12, Appl
3	1131	100.0	211	4	US-10-718-495-25	Sequence 25, Appl
4	1131	100.0	211	4	US-10-717-984-25	Sequence 25, Appl
5	1064	94.1	215	5	US-10-938-992-38	Sequence 38, Appl
6	1061	93.8	215	4	US-10-087-192-1446	Sequence 1446, Ap
7	1061	93.8	215	4	US-10-147-447-1	Sequence 1, Appli
8	1061	93.8	215	4	US-10-300-072-1	Sequence 1, Appli
9	1061	93.8	215	4	US-10-456-949-1	Sequence 1, Appli
10	1061	93.8	215	4	US-10-456-947-1	Sequence 1, Appli
11	1061	93.8	215	4	US-10-718-495-1	Sequence 1, Appli
12	1061	93.8	215	4	US-10-717-984-1	Sequence 1, Appli
13	1061	93.8	215	5	US-10-868-577A-63	Sequence 63, Appl
14	1061	93.8	215	5	US-10-868-549-22	Sequence 22, Appl
15	1061	93.8	215	5	US-10-938-992-74	Sequence 74, Appl
16	1059	93.6	214	3	US-09-214-881A-3	Sequence 3, Appli
17	1059	93.6	214	5	US-10-726-195-3	Sequence 3, Appli
18	1059	93.6	215	5	US-10-938-992-37	Sequence 37, Appl
19	1058	93.5	215	4	US-10-147-447-2	Sequence 2, Appli
20	1058	93.5	215	4	US-10-300-072-2	Sequence 2, Appli
21	1058	93.5	215	4	US-10-456-949-2	Sequence 2, Appli
22	1058	93.5	215	4	US-10-456-947-2	Sequence 2, Appli
23	1058	93.5	215	4	US-10-718-495-2	Sequence 2, Appli
24	1058	93.5	215	4	US-10-717-984-2	Sequence 2, Appli
25	1058	93.5	215	5	US-10-938-992-18	Sequence 18, Appl
26	1058	93.5	220	4	US-10-087-192-1443	Sequence 1443, Ap
27	1058	93.5	252	5	US-10-938-992-5	Sequence 5, Appli
28	1056	93.4	214	3	US-09-214-881A-1	Sequence 1, Appli
29	1056	93.4	214	5	US-10-726-195-1	Sequence 1, Appli
30	1056	93.4	221	5	US-10-938-992-40	Sequence 40, Appl
31	1054	93.2	214	3	US-09-214-881A-4	Sequence 4, Appli
32	1054	93.2	214	5	US-10-726-195-4	Sequence 4, Appli
33	1051	92.9	214	3	US-09-214-881A-5	Sequence 5, Appli
34	1051	92.9	214	5	US-10-726-195-5	Sequence 5, Appli
35	1045	92.4	216	4	US-10-147-447-18	Sequence 18, Appl
36	1045	92.4	216	4	US-10-300-072-18	Sequence 18, Appl
37	1045	92.4	216	4	US-10-300-072-24	Sequence 24, Appl
38	1045	92.4	216	4	US-10-456-949-18	Sequence 18, Appl
39	1045	92.4	216	4	US-10-456-947-6	Sequence 6, Appli
40	1045	92.4	216	4	US-10-456-947-10	Sequence 10, Appl
41	1045	92.4	216	4	US-10-718-495-18	Sequence 18, Appl
42	1045	92.4	216	4	US-10-718-495-24	Sequence 24, Appl
43	1045	92.4	216	4	US-10-717-984-18	Sequence 18, Appl
44	1045	92.4	216	4	US-10-717-984-24	Sequence 24, Appl
45	1045	92.4	216	5	US-10-938-992-1	Sequence 1, Appli

ALIGNMENTS

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US-10-300-072-25
; Sequence 25, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  APPLICANT:  Howland Shaw Warren, Jr.
;  APPLICANT:  Mitchell P. Fink
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
;  TITLE OF INVENTION:  AGENTS
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;  FILE REFERENCE: 3268.1001-005
;  CURRENT APPLICATION NUMBER: US/10/300,072
;  CURRENT FILING DATE:  2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: US 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-300-072-25

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Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHSDASVNFSEFSNKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKTHYERQMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYHPKIKGEHPGL 120
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Qy        121 SIGDVAKKLGEMWNNTAADDKQPGEKKAAKLKEKYEKDIAAYQAKGKPEAAKKGVVKAEK 180
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Qy        181 SKKKKEEEEDEEDEEDEEEEDEEDEEDDDDE 211
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; Sequence 12, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-12
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHSDASVNFSEFSNKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKTHYERQMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYHPKIKGEHPGL 120
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Qy        121 SIGDVAKKLGEMWNNTAADDKQPGEKKAAKLKEKYEKDIAAYQAKGKPEAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPGEKKAAKLKEKYEKDIAAYQAKGKPEAAKKGVVKAEK 180

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RESULT 3
US-10-718-495-25
; Sequence 25, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-25

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHSDASVNFSEFSNKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHSDASVNFSEFSNKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKTHYERQMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYHPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 SIGDVAKKLGEMWNNTAADDKQPGEKKAAKLKEKYEKDIAAYQAKGKPEAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPGEKKAAKLKEKYEKDIAAYQAKGKPEAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEDEEDEEDDDDE 211
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Db        181 SKKKKEEEEDEEDEEDEEEEDEEDEEDDDDE 211
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RESULT 4
US-10-717-984-25
; Sequence 25, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
;  FILE REFERENCE: 3258.1008-001
;  CURRENT APPLICATION NUMBER: US/10/717,984
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,846
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-717-984-25

  Query Match             100.0%;  Score 1131;  DB 4;  Length 211;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-71;
  Matches  211;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHSDASVNFSEFSNKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHSDASVNFSEFSNKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKTHYERQMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYHPKIKGEHPGL 120
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Qy        121 SIGDVAKKLGEMWNNTAADDKQPGEKKAAKLKEKYEKDIAAYQAKGKPEAAKKGVVKAEK 180
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RESULT 5
US-10-938-992-38
; Sequence 38, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
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L7 ANSWER 20 OF 32 DRUGU COPYRIGHT 2006 THE THOMSON CORP on STN
ACCESSION NUMBER: 2003-01232 DRUGU P
TITLE: HMGB1-targeted therapy ameliorates collagen-induced arthritis in mice.
AUTHOR: Kokkola R M J; Sundberg E; Tracey K J; Andersson U; Harris H E
CORPORATE SOURCE: Karolinska-Inst.
LOCATION: Stockholm, Swed.; Manhasset, N.Y., USA
SOURCE: Arthritis Rheum. (46, No. 9, Suppl., S566, 2002)
CODEN: ARHEAW ISSN: 0004-3591
AVAIL. OF DOC.: Karolinska Institutet, Stockholm, Sweden.
LANGUAGE: English
DOCUMENT TYPE: Journal
FIELD AVAIL.: AB; LA; CT
FILE SEGMENT: Literature
AB The effects of i.p. high mobility group box chromosomal protein 1 (**HMGB1**) **A-box** and anti-HMGB1 antibodies were investigated in an in-vitro study and in in-vivo studies in mice with collagen-induced CIA. **HMGB1 A-box** decreased production of proinflammatory **cytokines** induced by HMGB1 B-**box**. **HMGB1 A-box** and anti-HMGB1 antibodies ameliorated arthritis in-vivo in mice. In conclusion, the results show HMGB1 may be a future target for therapy of human arthritis an A-box and/or anti-HMGB1 antibodies could be sued as antagonists of excessive **cytokine** production in arthritis. (conference abstract: American College of Rheumatology 66th Annual Scientific Meeting and the Association of Rheumatology Health Professionals 37th Annual Scientific Meeting, New Orleans, Louisiana, USA, 2002).
AB The effects of i.p. high mobility group box chromosomal protein 1 (**HMGB1**) **A-box** and anti-HMGB1 antibodies were investigated in an in-vitro study and in in-vivo studies in mice with collagen-induced CIA. **HMGB1 A-box** decreased production of proinflammatory **cytokines** induced by HMGB1 B-**box**. **HMGB1 A-box** and anti-HMGB1 antibodies ameliorated arthritis in-vivo in mice. In conclusion, the results show HMGB1 may be a future target for therapy of human arthritis an A-box and/or anti-HMGB1 antibodies could be sued as antagonists of excessive **cytokine** production in arthritis. (conference abstract: American College of Rheumatology 66th Annual Scientific Meeting and the Association of Rheumatology Health Professionals. . .
ABEX. . . Methods DBA1/J mice were immunized with bovine collagen type II to induce CIA and were boosted on day 21, I.p. **HMGB1 A-box** or anti-HMGB1 antibodies were given for 7 days. Results In-vitro in mouse peritoneal macrophages, HMGB1 B-box-induced **TNF** production was decreased after preincubation with **HMGB1 A-box**. In-vivo, **HMGB1 A-box** or anti-HMGB1 antibodies treated mice showed lower mean arthritis indexes compared with controls. The number of affected paws and paws. . .

L7 ANSWER 19 OF 32 LIFESCI COPYRIGHT 2006 CSA on STN DUPLICATE 6
ACCESSION NUMBER: 2003:62793 LIFESCI
TITLE: HMGB1 as a cytokine and therapeutic target
AUTHOR: Yang, H.; Wang, H.; Czura, C.J.; Tracey, K.J.
CORPORATE SOURCE: Laboratory of Biomedical Science, North Shore-Long Island Jewish Research Institute, 350 Community Drive, Manhasset, NY 11030, USA; E-mail: hyang@nshs.edu
SOURCE: Journal of Endotoxin Research [J. Endotoxin Res.], (20020000) vol. 8, no. 6, pp. 469-472.
ISSN: 0968-0519.
DOCUMENT TYPE: Journal
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SUMMARY LANGUAGE: English
AB HMGB1 is an abundant nuclear and cytoplasmic protein present in mammalian cells. It is traditionally known as a DNA binding protein involved in maintenance of nucleosome structure and regulation of gene transcription. Beyond these intracellular roles, we recently discovered that HMGB1 is released from activated macrophages and functions as a late mediator of lethal endotoxemia. Addition of HMGB1 to macrophage cultures activates **cytokine** release. When released into the extracellular milieu, HMGB1 causes systemic inflammatory responses including acute lung injury, epithelial barrier dysfunction, and death. Passive immunization with anti-HMGB1 antibodies confers significant protection against lethality induced by LPS administration and sepsis caused by cecal perforation in mice. Truncation of HMGB1 into individual structural domains revealed that the **HMGB1 A box**, a DNA-binding motif, specifically antagonizes the activity of HMGB1 and rescues mice from lethal sepsis caused by cecal perforation. Thus, strategies that target HMGB1 with specific antibodies or antagonists have potential for treating lethal systemic inflammatory diseases characterized by excessive HMGB1 release.

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	SOURCE GeneReport for Unigene cluster: Hs.447630
Similar Genes in Other Organisms (According to [1]HomoloGene, [2]euGenes, [3]SGD and/or [4]MGD Oct 08 2005, with possible further links to Flybase and/or WormBase) *About Top*	--
Paralogs (Paralogs according to [1]HomoloGene and [2]Ensembl, Pseudogenes according to [3]pseudogene.org) *About Top*	**Paralogs** HMGB1[2] HMG1L10[2] **Pseudogenes** 6 related pseudogenes
SNPs/Variants (According to the NCBI SNP Database and UniProt, Genotyping Reagents from Applied Biosystems) *About Top*	--
Disorders & Mutations (in which this Gene is Involved, According to OMIM, UniProt, Genatlas, GeneTests, HGMD, GAD, GDPInfo, BCGD, and/or TGDB.) *About Top*	--
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Research Articles (in PubMed. Associations of this gene to articles via bioalma, HGNC, Entrez Gene, UniProt, and/or GAD)	**1 PubMed article**: ***the following papers are cited by 2 GeneCards sources:*** • Mapping and molecular characterization of five HMG1-related DNA sequences. R **Search PubMed for:** **Gene symbol** **Aliases**

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=> d his

     (FILE 'HOME' ENTERED AT 12:43:21 ON 28 APR 2006)

     FILE 'STNGUIDE' ENTERED AT 12:43:55 ON 28 APR 2006
L1             0 S HMG1L1
L2             0 S HMG? (A) A (A) BOX

     FILE 'DISSABS, 1MOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,
     COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN,
     PAPERCHEM2, PASCAL, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT, ADISNEWS,
     ANABSTR, ANTE, AQUALINE, BIOENG, BIOSIS, ...' ENTERED AT 12:54:39 ON 28
     APR 2006
L3            31 S HMG1L1
L4             8 S L3 (S) (CYTOKINE OR TNF)
L5           296 S HMG? (A) A (A) BOX
L6            41 S L5 (S) (CYTOKINE OR TNF)
L7            32 DUP REM L6 (9 DUPLICATES REMOVED)

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     PAPERCHEM2, PASCAL, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT, ADISNEWS,
     ANABSTR, ANTE, AQUALINE, BIOENG, BIOSIS, ...' ENTERED AT 13:07:04 ON 28
     APR 2006

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